

Steven M. Ruben
Appl. No. 10/662,429

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FROM: C. Harner Total Pages Including Transmittal Sheet 7

COMMENTS: Bol this is the patch for AIM-I (previously
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FROM: C. Harrow

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COMMENTS: Bol- this is the packet for AIM-I (previously
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 NAME (ID NUMBER) 3098504
 START TIME MAR-14-96 08:32
 PAGES TRANSMITTED 866 TRANSMISSION MODE EMNR
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 SECURITY ON MAILBOX OFF
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 LAST SUCCESSFUL PAGE 866

CARELLA BYRNE, BAIN, GILFILLAN,
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 6 Becker Farm Road
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 (201) 994-1700
 (201) 994-1744 (FAX)

DATE: March 14, 1996

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301,309-8513

FROM: S. Hermann

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 NAME (ID NUMBER) 3098524
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FROM: S. Harned Total Pages Including Transmittal Sheet 71

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Figure 1

Nucleotide and Amino Acid Sequence of AEM-I

-51	GGCACCAGCGGCTGCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCTATGGCTATG	8
-16	CCGTGCTCGCGACGGACCGACTGAATGTCGTGCTGAGCTGTCCAGTACCGATAC	3
	M A M	
9	ATGGAGTCCAGGGGGACCCAGCCTGGGACAGACCTGGTGGTGTGATCGTATCTTCACA	68
4	TACCTCCAGTCCCCCTGGGTCGGACCTGTCTGGACCGACGACTAGCACTAGAAGTGT	23
	M E V Q G G P S L G Q T C V L I Y I F T	
69	GTGCTCTGAGTCTCTCTGTGTGGCTGTAACCTACGTGTACTTACCAACGAGGTGAAG	128
24	CACGAGGACGTGAGAGAGACACACCGACATTGAATGCACATCAAAATGGTTGCTCGACTTC	43
	V L L Q S L C Y A V T Y Y Y F T N E L K	
129	CAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTCTTAAAGAAGATGACAGT	188
44	GTCTACGTCTGTTCATGAGGTTTTACCGTAACGAAACAAGAAATTTCTTCTACTGTCA	63
	Q M Q D K Y S K S G I A C F L K E D D S	
189	TATTGGGACCCCAATGACGAAGACAGTATGAACAGCCCTGCTGGCAAGTCAAGTGGCAA	248
64	ATAACCTGGGGTACTGCTTCTCTCACTTGTGGGGACGACCGTTCAAGTTCACCGTT	83
	Y N D P N D E E S M N S P C W Q V K N Q	
249	CTCCGTGAGTCTGTTAGAAAGATCATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT	308
84	GAGGCAGTCGAGCAATCTTTCTACTAAAACTCTTGAGACTCTTTGGTAAAGATGTCAA	103
	L R Q L V R K M I L R T S E E T I S T V	
309	CAAGAAAAGCAAAAATATTTCTCCCTAGTCAGAGAAAGAGGTCTCAGAGAGTAGCA	368
104	GTCTTTTCGTTGTTTTATAAGAGGGGATCACTCTCTTCTCAGGAGTCTCTCATCGT	123
	Q E K Q Q N I S P L V R E R G P Q R V A	
369	GCTCATAACTGGGACGAGGAAAGCAAGCAACATGCTTCTCCAACTCCAAGAAT	428
124	CGAGTGTATTGACCTGGTCTCTTCTTCTGTTGTAAACAGAGAGGTTGAGGTTCCTA	143
	A H I T G T R G R S N T L S S P N S K N	
429	GAAAAGGCTCTGGGCGCAAAATAAACTCTGGGAATCATCAAGGAGTGGGCATTCTTC	488
144	CTTTCCGAGACCCGGCGTTTATTTGAGGACCTTAGTAGTCTCACCCTAAGTAAG	163
	E K A L G R K I N S N E S S R S G H S F	
	CTGAGCACTTGCACTTGAGGAATGGTGAAGTGGTCATCCATGAAAAAGGGTTTTACTAC	

Figure 1 (con'd)

489	-----	548
164	GACTCGTTGAACGTGAACCTCCTTACCACCTTGACCAGTAGGTACTTTTCCCAAAATGATG L S M L H L R N G E L V I H E K G F Y Y	583
549	-----	608
184	ATCTATTCCCAACATACCTTTGATTTGAGGAGGAAATAAAAGAAAACACAAAGAACGAC TAGATAAGGTTTGTATGAAAGCTAAAGTCCTCTTTATTTTCTTTGTGTTTCTTGTG I Y S Q T Y F R F Q E E I K E N T K N D	203
629	-----	668
204	AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCATATTGTTGATG TTTGTTTACCAGTTATATAAATGTTTATGTGTTCAATAGGACTGGGATATAACAACCTAC K Q M V Q Y I Y K Y T S Y P O P I L L M	223
669	-----	728
224	AAAAGTGTAGAAATAGTTGTTGGTCTAAAGATGCAGAAATGGACTCTATTCATCTAT TTTTCAGGATCTTTATCAACAACCCAGATTTCTACGTCTTATACCTGAGATAAGGTAGATA K S A R M S C W S K D A E Y G L Y S I Y	243
729	-----	788
244	CAAGGGGAATATTGAGCTTAAGGAAAATGACAGAAATTTTGTCTGTAAACAAATGAG GTCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC Q G G I F E L K E N D R I F V S V T N E	253
789	-----	848
264	CACCTGATAGACATGACCATGAAGCCAGTTTTCGGGGCCTTTTAGTTGGCTAACTG GTGACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGAAAAATCAACCGATTGAC H L I D M D H E A S F F G A F L V G	881
849	-----	908
	ACCTGGAAAGAAAAAGCAATAACCTCAAAGTGACTATTGAGTTTCAGGATGATACCTA TGGACCTTTCTTTTCTGTTATTGGAGTTTCACTGATAAGTCAAAAGTCTACTATGTGAT	
909	-----	968
	TGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAC ACTTCTACAAAGTTTCTAGACTGGTCTTGTGTTGTTGTTCTTTGTTCTTTGTTTTTG	
969	-----	1028
	CTCTATGCAATCTGAGTAGAGCAGCCACAACCAAAAAATCTACAACACACACTGTTCTG GAGATACGTTAGACTCATCTCTCGGTGTTGTTTTTAAAGATGTTGTGTGTGACAAGAC	
1029	-----	1088
	AAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGATCTTCAGGACTCTACCT TTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTTCTAGAAAGTCTGAGATGGA	
1089	-----	1148
	CATATCAGTTTGTAGCAGAAATCTAGAAGACTGTGAGCTTCAAAACATTAAATGCAATGG GTATAGTCAACGATCTCTTTAGATCTTCTGACAGTCAAGGTTTGTAAATTACGTTACC	

Figure 1 (con'd)

1149 TTAACATCTTCTGCTTTATAATCTACTCTTGTAAAGACTGTAGAAGAAAGCGCAACA
 1208 AATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTCCGCTTTT
 1209 TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCCTCCAGTTTCCCTAAGGGACAACATC
 1268 AGGTAGAGAGTTCATCAGATAGTGCATCATCGGAGGTCCAAAGGAATTCCCTGTTGTAG
 1269 CTTAAGTCAAAAGAGAGAGAGGACCACTAAAAGATCCAGTTTGCCTGGTGCAAGTGGC
 1328 GAATTCAGTTTTCTCTCTTCTCGTGATTTTCTAGCGTCAAACGGACCACGTCACCG
 1329 TCACACCTGTAATCCCAACATTTGGGAACCAAGTGGGTAGATCAGGAGATCAAGAGA
 1388 AGTGTGGACATTAGGGTTGTAAAACCTTGGGTCCACCCATCTAGTGCTCTAGTTCTCT
 1389 TCAAGACCATAGTGACCAACATAGTGAACCCCATCTCTACTGAAAGTGCAAAAATTAGC
 1448 AGTTCTGGTATCACTGGTTGTATCACTTTGGGTAGAGATCACTTCACGTTTTTAATCG
 1449 TGGGTGTGTTGGACATGCCTGTAGTCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCG
 1508 ACCCACAACCGTGACGGACATCAGGTCGATGAAGTCTCCGACTCCGTCTCTTAGC
 1509 TTTGAACCCGGGAGGAGAGGTTGCAGTGTGGTGAGATCATGCCACTACACTCCAGCCTG
 1568 AAACCTTGGGCCCTCCGTCTCAACGTCACCACTCTAGTACGGTGATGTGAGGTCCGAC
 1569 GCGACAGAGCGAGACTTGTTTTT
 1591 CGCTGTCTCGCTCTGAACCAAAG

Figure 2

Alignment of AIM-I to Human Fas Ligand
(Similarity = 48.594 % Identity = 22.892 %)

```

4 MEVQGGPSLGQTCLVIVFVL.....LQSLCVAVTV 36
  :: ..... 1 :: ..... 1 .....
15 VSSASSPWAPPSTVLCPSTVPRTPGQRTPPPPPPPPPPPPPPPPP 64
37 YFTNELKQKQKYSKSGACFLKEDSYMDPNDDESHNSPCNQVKQLRQ 86
  :: ..... 1 :: ..... 1 :: ..... 1 :: .....
65 PLP..LPPLKRGHNSGLCLV...FFAVLVAVLGIGLGMFQL.FHLQK 109
87 LYRQKELRTSEETSTVQEKQONISPLVRERGPRVAAHETGTRGRSNTL 136
  :: ..... 1 :: ..... 1 :: ..... 1 :: .....
110 ELAELRESTSQMHTASSLEKQIGHSPPEKKELRKVAHLT...GKSNSR 156
137 SSPNSKNEKALGRICNSWESSRSQHSFLSNLHLRNGELVHEKGFYYEYS 186
  :: ..... 1 :: ..... 1 :: ..... 1 :: .....
157 SAPLEWEDTY.....GIVLSGVKYKKGGIVINETGLYFVYS 193
187 QTYFRFQEEIKENTKNDKQWQYIYKYS.YPDPIILMKSAKNSCKSKDA 235
  :: ..... 1 :: ..... 1 :: ..... 1 :: .....
194 KVFYR.....GQSCNNIPLSHKVMKNSKYPQDIVMEGKMSYCTTGQ 237
236 EYGLYSIYQGGEFELKENDREFVSVTNEHLIDMDHEASFFGAFV 280
  :: ..... 1 :: ..... 1 :: ..... 1 :: .....
238 MVAR..SSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKI 281

```


Figure 1 (con'd)

1249	TTAACATCTTCTGTCTTTATAATCTACTCTTGTAAAGACTGTAGAAGAAAGCGCAACA	1208
	AAATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTCGGCTTGT	
1209	TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCTCCAGGTTTCTTAAGGGACAACATC	1268
	AGGTAGAGAGTTCATCACATAGTGTCACTATCGGAGGTCCAAAGGAATTCCTGTTGTAG	
1269	CTTAAGTCAAAAGAGAGAGAGAGGACCACTAAAAGATCGCAGTTTGCCTGGTGCACTGGC	1328
	GAATTCAGTTTTCTCTCTTCTCGTGGTGATTTTCTAGCGTCAAACGGACCACGTCACTG	
1329	TCACACCTGTAATCCCAACATTTGGGAACCAAGTGGGTAGATCAGGATCAAGAGA	1388
	AGTGTGGACATTAGGTTTGTAAAACCTTGGGTCCACCCATCTAGTGCTCTAGTTCTCT	
1389	TCAGACCATAGTGACCAACATAGTGAACCCCATCTCTACTGAAAGTGCAAAAATTAGC	1448
	AGTTCTGGTATCACTGGTTGTATCACTTGGGGTAGAGATGACTTTCAGTTTTTAATCG	
1449	TGGGTGTGTTGGCAGATGCTGTAGTCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCG	1508
	ACCCACACAACCGTGTACGGACATCAGGTCGATGAAGTCTCCGACTCGTCTCTTAGC	
1509	TTTGAACCCGGGAGGAGAGGTTGAGTGTGGTGAGATCATGCCACTACACTCCAGCCTG	1568
	AAACTTGGGCECTCCGTCTCCAACGTCAACCACTCTAGTACGGTGATGTGAGGTCCGAC	
1569	GCGACAGAGCGAGACTTGGTTTC	1591
	CGCTGTCTCGCTCTGAACCAAAG	

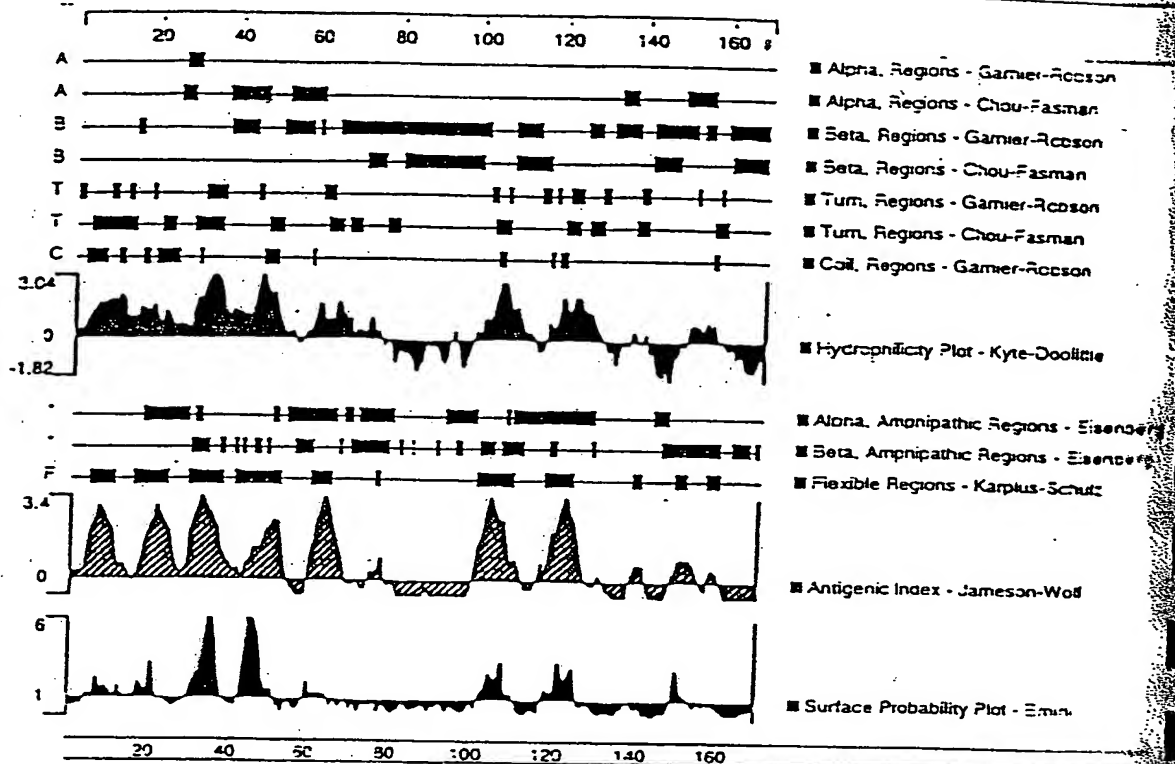
Denoting σ : Side (with solid black) residues that match $\Delta\epsilon_{\text{Alp}}^{\text{Alp}}$ exactly.

نشانی

do you have such a Fig
for A.M.I (Farligand)?

if to please fax to me

Thanks
Charlie



Steve

do you have such a
Fig for AIM-I (Foligant)?

if so please fax to me

Thanks

Charlie

Alignment Report of Unrooted 1 Clustal method with PAM50 residue weight 200.
 Thursday, March 14, 2006 11:10 AM

Page 1

	10	20	30		
1	MAAMMEVQGGIPIS	---	GGQCVL	VVFV	ALN 1
1	MQGPMNYPCLG	FWVSSA	SSWA	PPG	FAS LIGAND U06948.pcp
1	---	---	---	---	U06948.pcp
1	---	---	---	---	U06948.pcp
	40	50	60		
26	UQSLVAVTYVY	NEELKQNGQKYSK	SGIA	ALN 1	
31	PCPSLPPRG	---	PDQRPPPPPP	PPV	FAS LIGAND U06948.pcp
2	---	---	---	SSMT	U06948.pcp
9	LP RV	---	---	---	U06948.pcp
	70	80	90		
56	CFKEDSYWDIPN	DEESMINS	SCWQIVK	WQ	ALN 1
57	---	---	---	---	FAS LIGAND U06948.pcp
12	---	---	---	---	U06948.pcp
17	---	---	---	---	U06948.pcp
	100	110	120		
86	PLVRKMR	RSSE	SSVCEK	QCN	ALN 1
85	---	---	---	---	FAS LIGAND U06948.pcp
12	---	---	---	---	U06948.pcp
21	---	---	---	---	U06948.pcp
	130	140	150		
126	ETPQPVAAH	---	---	---	ALN 1
124	---	---	---	---	FAS LIGAND U06948.pcp
62	---	---	---	---	U06948.pcp
34	CLP	GVG	---	---	U06948.pcp
	160	170	180		
146	ALGLRKN	---	---	---	ALN 1
143	---	---	---	---	FAS LIGAND U06948.pcp
88	---	---	---	---	U06948.pcp
0	---	---	---	---	U06948.pcp
	190	200	210		
167	LNLRN	---	---	---	ALN 1
172	---	---	---	---	FAS LIGAND U06948.pcp
177	---	---	---	---	U06948.pcp
92	---	---	---	---	U06948.pcp
	220	230	240		
157	KEN	---	---	---	ALN 1
202	---	---	---	---	FAS LIGAND U06948.pcp
146	---	---	---	---	U06948.pcp
177	---	---	---	---	U06948.pcp



HGS

Facsimile Cover Sheet

Human Genome Sciences, Inc.
9620 Medical Center Drive, #300
Rockville, MD 20850-3338
(301) 309-8504 (301) 340-7159 Fax



DATE: 3-14-96

TO: Charles Herron

FAX #: 201-994-1744

FROM: Steve Ruben

COMMENTS:

Number of Pages (including cover): 4

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201001/11/1/3/7

Page 1

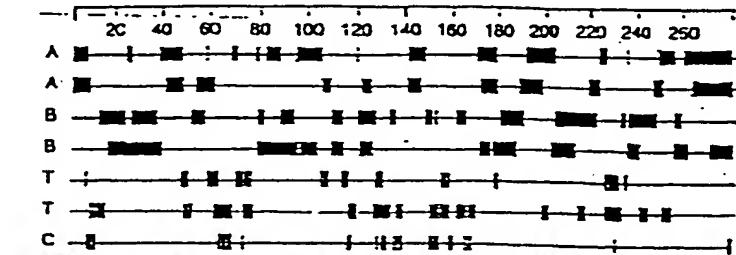
Alignment Report of Unlabeled, using Clustal method with PAM250 residue weight table.
Thursday, March 14, 1996 11:16 AM

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1	M Q Q P M N Y P C P Q	- - - - - W V D S S A	S S W A P B G S V P	FAS LIGAND	U06948.pep
1	M	- - - - -	T P P E R L F I	unfa.pep	
1	M	- - - - -	- - - - -	unfb.pep	
	40	50	60		
26	L Q S L C I V A V T Y V Y P T N E L K Q H Q Q K Y S K S I G I A	AIM 2			
31	P C P S C G P R G	- - - - - P Q R R P P P P P P P V S P L P	FAS LIGAND	U06948.pep	
2	- - - - -	- - - - - S T E S M I R D V E	unfa.pep		
9	L P R V C G T T	- - - - -	- - - - -	unfb.pep	
	70	80	90		
56	C F L K L E D C S Y W D P N D E E S M I N S P C W Q V K W Q L R	AIM 1			
57	- - - - - P P S Q P L P L P P L T P L K K K D H N T N L W L P V V	FAS LIGAND	U06948.pep		
12	- - - - - L A E E A L P	- - - - - K K T G G P Q G S R R C L	unfa.pep		
17	- - - - -	- - - - -	- - - - -	unfb.pep	
	100	110	120		
86	Q L V R K M	- - - - - R T S E E L	- - - - - S V Q E K Q Q N S P L V R	AIM 1	
95	F E M V L V A	- - - - - V G M G L G - M Y Q L F H L O K E A E L R	FAS LIGAND	U06948.pep	
32	- - - - - S L E S E L	- - - - - I V A I G A T L Y C L L M F G V G P Q R E	unfa.pep		
21	L L G L L V	- - - - -	- - - - - L P C A Q	unfb.pep	
	130	140	150		
116	Z R G F Q R V A A E E T G T	R G R S N T L S I S P N S K N S K	AIM 1		
114	E P T - N Q S L	K V S S F E K Q T A N D S T P S E K K E P R	FAS LIGAND	U06948.pep	
62	E S P R D L S L	- - - - - S P L A Q A V K S S S K T S S D - - - - - K	unfa.pep		
34	C L P - C V I G	- - - - - P S A A O T A I R Q L P K M H L A H S T L K	unfb.pep		
	160	170	180		
146	A L G I R K E N S I	- - - - - W E S S S S S G H S F L S I N	AIM 1		
143	S V A H L T G N P E	- - - - - S R S I P L E W E D T Y G T A L I - S G	FAS LIGAND	U06948.pep	
88	S V A H V I V A N P Q A E G Q	- - - - - L Q W L N R R I A N A L L A N G	unfa.pep		
63	P A A H L T G D P	- - - - - S K Q N S L L W R A N T D R A F L Q D I G	unfb.pep		
	190	200	210		
167	L H L R N G R L V I H E K	G E Y Y I Y S Q I T Y F R I Q I E E	AIM 1		
172	V K Y K K G G L V - N E T	G L Y F V Y S K V Y F R C Q S C I N	FAS LIGAND	U06948.pep	
117	V I E L R D N Q L V V P S E G	- - - - - Y L - Y S Q V L F K G G G C	unfa.pep		
52	F S L I S I N N S L V N T S G	- - - - - Y F V Y S O V V F S C K A Y S	unfb.pep		
	220	230	240		
157	K E N T R N D K Q M V Q Y - Y K Y T S I	- - - - - Y P D P L E L M K S I	AIM 1		
202	N Q P - - - - - N H K V Y M R N S K Y P E D L V L M E E	FAS LIGAND	U06948.pep		
146	- - - - - P S T E V L L T H - - - - - S R - A V S Y Q T K V N L L S A	unfa.pep			
122	P K A P S S P - - - - - L A E E V C - - - - - P S S Q Y P F E V P - - - - - S S	unfb.pep			

AIM 1

Thursday, March 14, 1996 11:18 AM

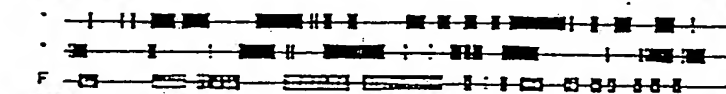
Page 1



■ Alpha, Regions - Garner-Robson
 ■ Alpha, Regions - Chou-Fasman
 ■ Beta, Regions - Garner-Robson
 ■ Beta, Regions - Chou-Fasman
 ■ Turn, Regions - Garner-Robson
 ■ Turn, Regions - Chou-Fasman
 ■ Coil, Regions - Garner-Robson



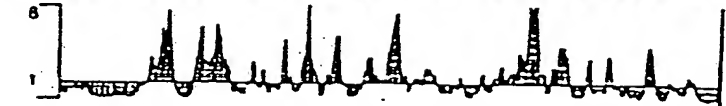
■ Hydrophobicity Plot - Kyte-Doolittle



■ Alpha, Amphipathic Regions - Eisenberg
 ■ Beta, Amphoteric Regions - Eisenberg
 ■ Flexible Regions - Karplus-Schut



■ Antigenic Index - Jamieson-Wolf



■ Surface Probability Plot - Emini

40 60 80 100 120 140 160 180 200 220 240 260 280

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